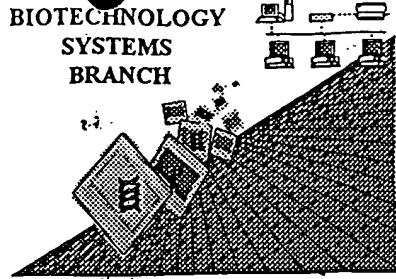


m.m

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/903,325

Source: OIPE

Date Processed by STIC: 7/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/903,325

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</u>
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

Re-RUA

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,325

DATE: 07/25/2001
TIME: 14:13:59

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07252001\I903325.raw

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: De Robertis, Edward M.
Bouwmeester, Tewis
8 (ii) TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
Factors

11 (iii) NUMBER OF SEQUENCES: 10

13 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Majestic, Parsons, Siebert & Hsue
16 (B) STREET: Four Embarcadero Center, Suite 1100
17 (C) CITY: San Francisco
18 (D) STATE: California
19 (E) COUNTRY: U.S.A.
20 (F) ZIP: 94111-4106

21 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US/09/903,325

30 (B) FILING DATE: 11-Jul-2001

31 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US 60/020,150

35 (B) FILING DATE: 20-JUN-1996

36 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Siebert, J. Suzanne
39 (B) REGISTRATION NUMBER: 28,758

40 (C) REFERENCE/DOCKET NUMBER: 3100.002US1

41 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 415/248-5500

44 (B) TELEFAX: 415/362-5418

45

ERRORED SEQUENCES

330 (2) INFORMATION FOR SEQ ID NO: 5:

332 (i) SEQUENCE CHARACTERISTICS:

333 (A) LENGTH: 979 amino acids

334 (B) TYPE: amino acid

335 (D) TOPOLOGY: linear

337 (ii) MOLECULE TYPE: peptide

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

341 Met Leu Leu Leu Phe Arg Ala Ile Pro Met Leu Leu Leu Gly Leu Met
342 1 5 10 15 Val Leu Gln Thr Asp Cys Glu Ile Ala Gln Tyr Tyr Ile Asp Glu Glu

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,325

DATE: 07/25/2001
TIME: 14:13:59

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07252001\I903325.raw

345	20	25	30
347	Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe		
348	35	40	45
350	Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe		
351	50	55	60
353	Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly-Gln Leu Ser Ile		80
354	65	70	75
356	Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys		95
357	85	90	
359	Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu		
360	100	105	110
362	Leu Asn Val Lys Val Glu Val Arg Asp Ile Asn Asp His Ser Pro His		
363	115	120	125
365	Phe Pro Ser Glu Ile Met His Val Glu Val Ser Glu Ser Ser Val		
366	130	135	140
368	Gly Thr Arg Ile Pro Leu Glu Ile Ala Ile Asp Glu Asp Val Gly Ser		
369	145	150	155
371	Asn Ser Ile Gln Asn Phe Gln Ile Ser Asn Asn Ser His Phe Ser Ile		160
372	165	170	175
374	Asp Val Leu Thr Arg Ala Asp Gly Val Lys Tyr Ala Asp Leu Val Leu		
375	180	185	190
377	Met Arg Glu Leu Asp Arg Glu Ile Gln Pro Thr Tyr Ile Met Glu Leu		
378	195	200	205
380	Leu Ala Met Asp Gly Gly Val Pro Ser Leu Ser Gly Thr Ala Val Val		
381	210	215	220
383	Asn Ile Arg Val Leu Asp Phe Asn Asp Asn Ser Pro Val Phe Glu Arg		240
384	225	230	235
386	Ser Thr Ile Ala Val Asp Leu Val Glu Asp Ala Pro Leu Gly Tyr Leu		
387	245	250	255
389	Leu Leu Glu Leu His Ala Thr Asp Asp Asp Glu Gly Val Asn Gly Glu		
390	260	265	270
392	Ile Val Tyr Gly Phe Ser Thr Leu Ala Ser Gln Glu Val Arg Gln Leu		
393	275	280	285
395	Phe Lys Ile Asn Ser Arg Thr Gly Ser Val Thr Leu Glu Gly Gln Val		
396	290	295	300
398	Asp Phe Glu Thr Lys Gln Thr Tyr Glu Phe Glu Val Gln Ala Gln Asp		
399	305	310	315
401	Leu Gly Pro Asn Pro Leu Thr Ala Thr Cys Lys Val Thr Val His Ile		320
402	325	330	335
404	Leu Asp Val Asn Asp Asn Thr Pro Ala Ile Thr Ile Thr Pro Leu Thr		
405	340	345	350
407	Thr Val Asn Ala Gly Val Ala Tyr Ile Pro Glu Thr Ala Thr Lys Glu		
408	355	360	365
410	Asn Phe Ile Ala Leu Ile Ser Thr Thr Asp Arg Ala Ser Gly Ser Asn		
411	370	375	380
413	Gly Gln Val Arg Cys Thr Leu Tyr Gly His Glu His Phe Lys Leu Gln		400
414	385	390	395
416	Gln Ala Tyr Glu Asp Ser Tyr Met Ile Val Thr Thr Ser Thr Leu Asp		
417	405	410	415

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,325

DATE: 07/25/2001
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Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07252001\I903325.raw

419 Arg Glu Asn Ile Ala Ala Tyr Ser Leu Thr Val Val Ala Glu Asp Leu
 420 420 425 430
 422 Gly Phe Pro Ser Leu Lys Thr Lys Lys Tyr Tyr Thr Val Lys Val Ser
 423 435 440 445
 425 Asp Glu Asn Asp Asn Ala Pro Val Phe Ser Lys Pro Gln Tyr Glu Ala
 426 450 455 460
 428 Ser Ile Leu Glu Asn Asn Ala Pro Gly Ser Tyr Ile Thr Thr Val Ile
 429 465. 470 475 480
 431 Ala Arg Asp Ser Asp Ser Asp Gln Asn Gly Lys Val Asn Tyr Arg Leu
 432 485 490 495
 434 Val Asp Ala Lys Val Met Gly Gln Ser Leu Thf-Thr Phe Val Ser Leu
 435 500 505 510
 437 Asp Ala Asp Ser Gly Val Leu Arg Ala Val Arg Ser Leu Asp Tyr Glu
 438 515 520 525
 440 Lys Leu Lys Gln Leu Asp Phe Glu Ile Glu Ala Ala Asp Asn Gly Ile
 441 530 535 540
 443 Pro Gln Leu Ser Thr Arg Val Gln Leu Asn Leu Arg Ile Val Asp Gln
 444 545 550 555 560
 446 Asn Asp Asn Cys Pro Val Ile Thr Asn Pro Leu Leu Asn Asn Gly Ser
 447 565 570 575
 449 Gly Glu Val Leu Leu Pro Ile Ser Ala Pro Gln Asn Tyr Leu Val Phe
 450 580 585 590
 452 Gln Leu Lys Ala Glu Asp Ser Asp Glu Gly His Asn Ser Gln Leu Phe
 453 595 600 605
 455 Tyr Thr Ile Leu Arg Asp Pro Ser Arg Leu Phe Ala Ile Asn Lys Glu
 456 610 615 620
 458 Ser Gly Glu Val Phe Leu Lys Gln Leu Asn Ser Asp His Ser Glu
 459 625 630 635 640
 461 Asp Leu Ser Ile Val Val Ala Val Tyr Asp Leu Gly Arg Pro Ser Leu
 462 645 650 655
 464 Val Ala Asn Arg Met His Ala Glu Tyr Glu Arg Asp Leu Val Asn Arg
 E--> 465 660 665 670
 467 Ser Ala Thr Leu Ser Pro Gln Arg Ser Ser Ser Arg Tyr Gln Glu Phe
 E--> 468 675 680 685 690 695 700 705 710
 470 Asn Tyr Ser Pro Gln Ile Ser Arg Gln Leu His Pro Ser Glu Ile Ala
 E--> 471 690 695 700 705 710 715
 E--> 473 Thr Thr Phe 705
 780 (2) INFORMATION FOR SEQ ID NO: 9:
 782 (i) SEQUENCE CHARACTERISTICS:
 783 (A) LENGTH: 325 amino acids
 784 (B) TYPE: amino acid
 785 (D) TOPOLOGY: linear
 787 (ii) MOLECULE TYPE: peptide
 789 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 791 Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Arg Ala Gly Leu
 792 1 5 10 15
 E--> 794 Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
 795 20 25 30
 797 Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp

*marked
no.
(see item 3
on Exam Summary
sheet)*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,325

DATE: 07/25/2001
TIME: 14:13:59

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07252001\I903325.raw

798	35	40	45
800	Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn		
801	50	55	60
803	Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys		80
804	65	70	75
806	Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys		95
807	85	90	
809	Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys		
810	100	105	110
812	Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His		
813	115	120	125
815	Ser Trp Pro Glu Asn Leu Ala Cys Glu Leu Pro Val Tyr Asp Arg		
816	130	135	140
818	Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp		160
819	145	150	155
821	Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu		175
822	165	170	
824	Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg		
825	180	185	190
827	Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr		
828	195	200	205
830	Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys		
831	210	215	220
833	Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser		240
834	225	230	235
836	Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile		255
837	245	250	
839	Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly		
840	260	265	270
842	Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg		
843	275	280	285
845	Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser		
846	290	295	300
848	Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro		320
849	305	310	
851	Arg Gln Ala Arg Asn		
852	325		

7/25/01

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/903,325

DATE: 07/25/2001
TIME: 14:14:00

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07252001\I903325.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:465 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:473 M:203 E: No. of Seq. differs, LENGTH:Input:979 Found:707 SEQ:5
L:792 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9

7/25/01